

Figure 1

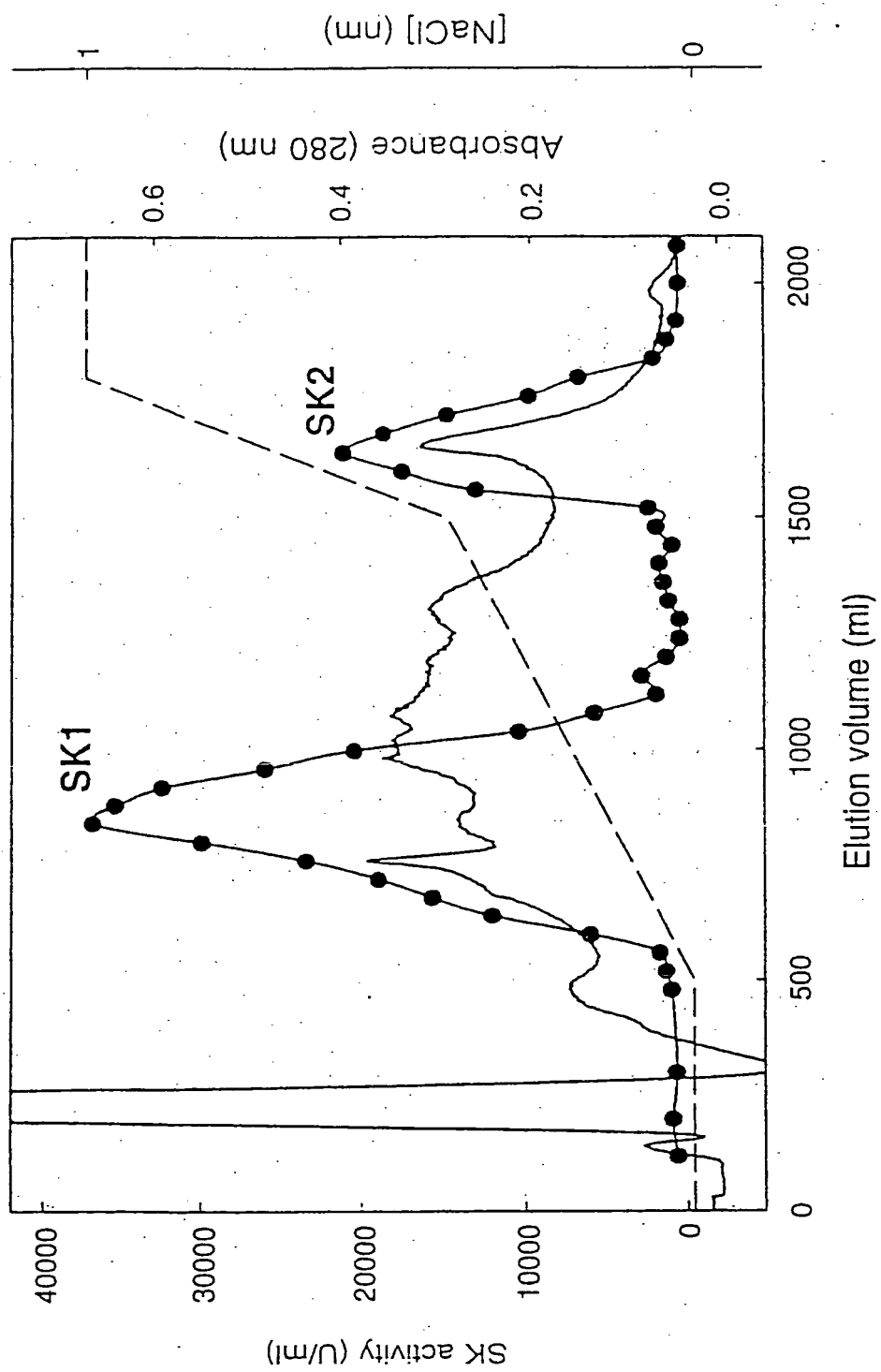
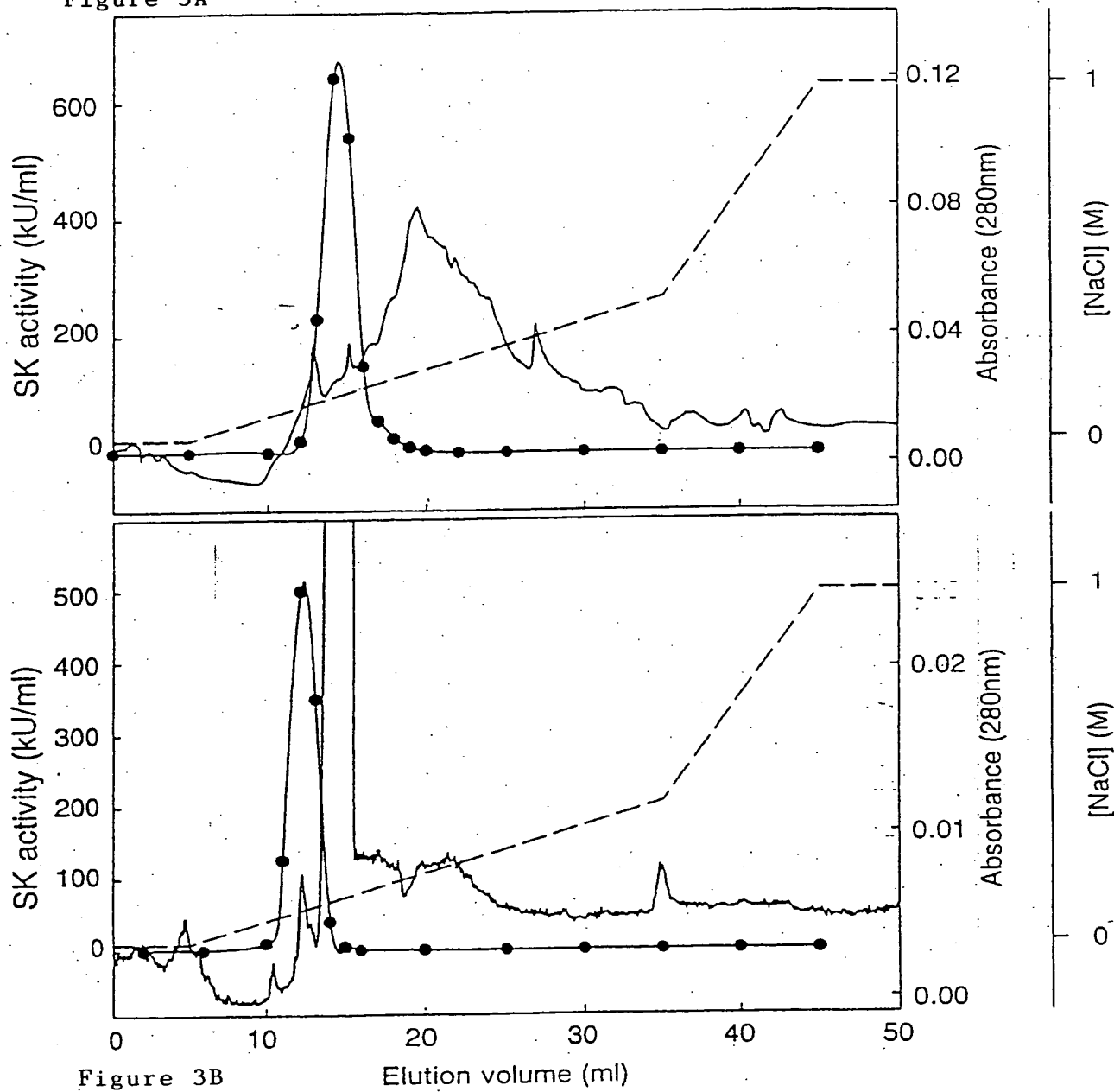


Figure 2

Figure 3A



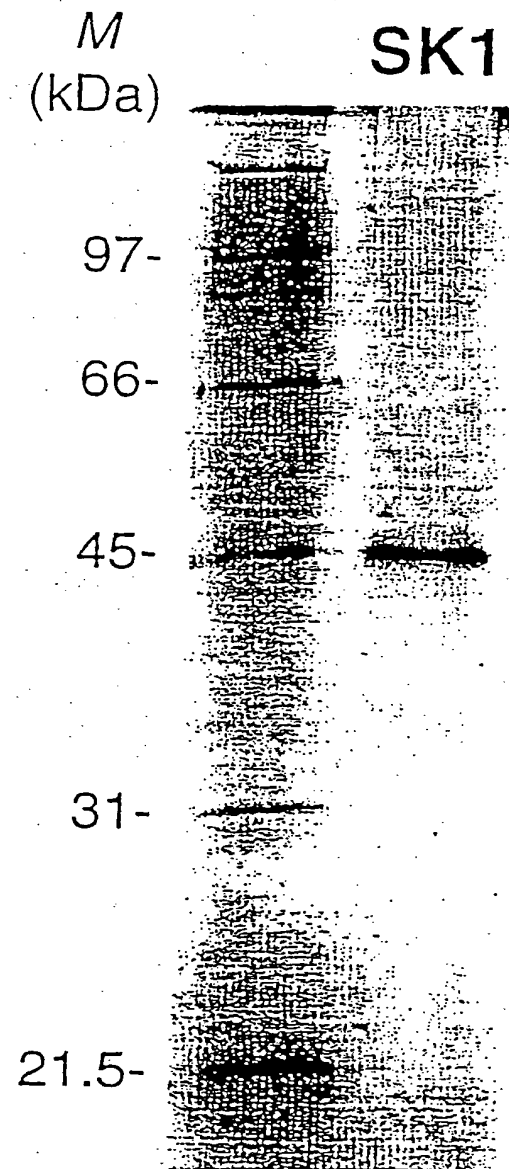


Figure 4

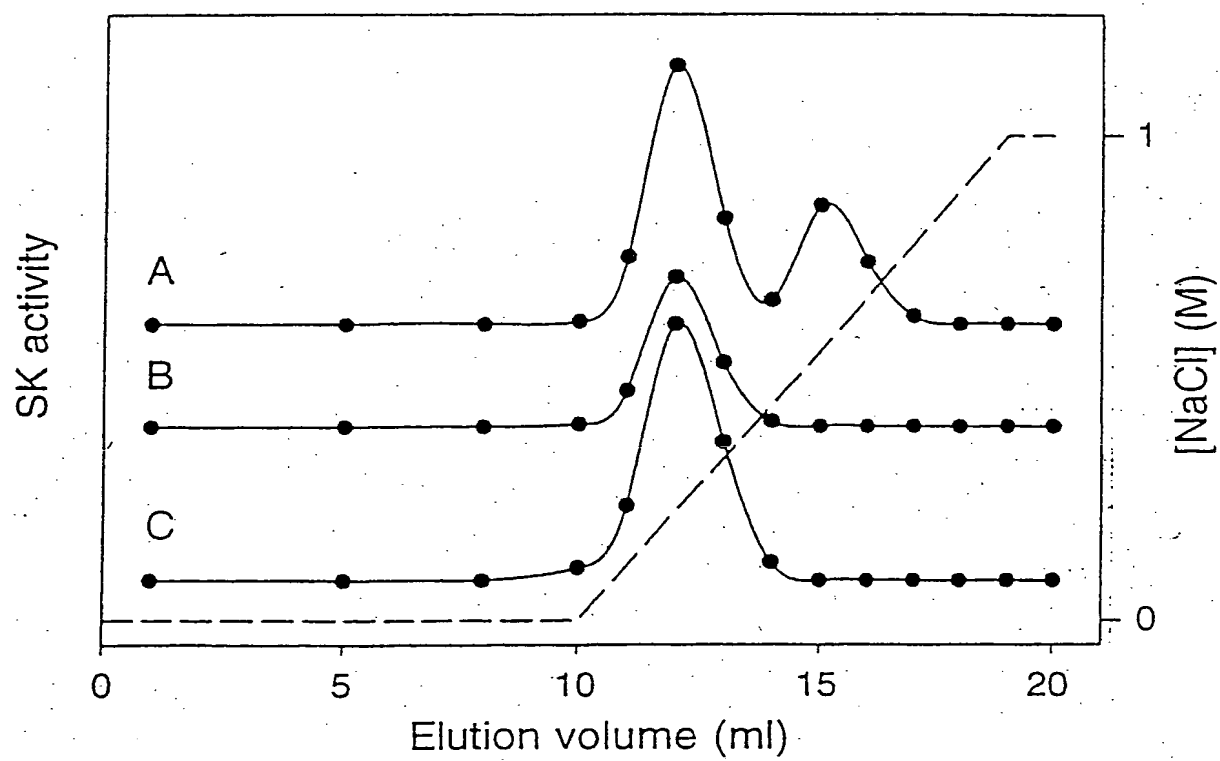


Figure 5

# Cloning of HUVEC SK

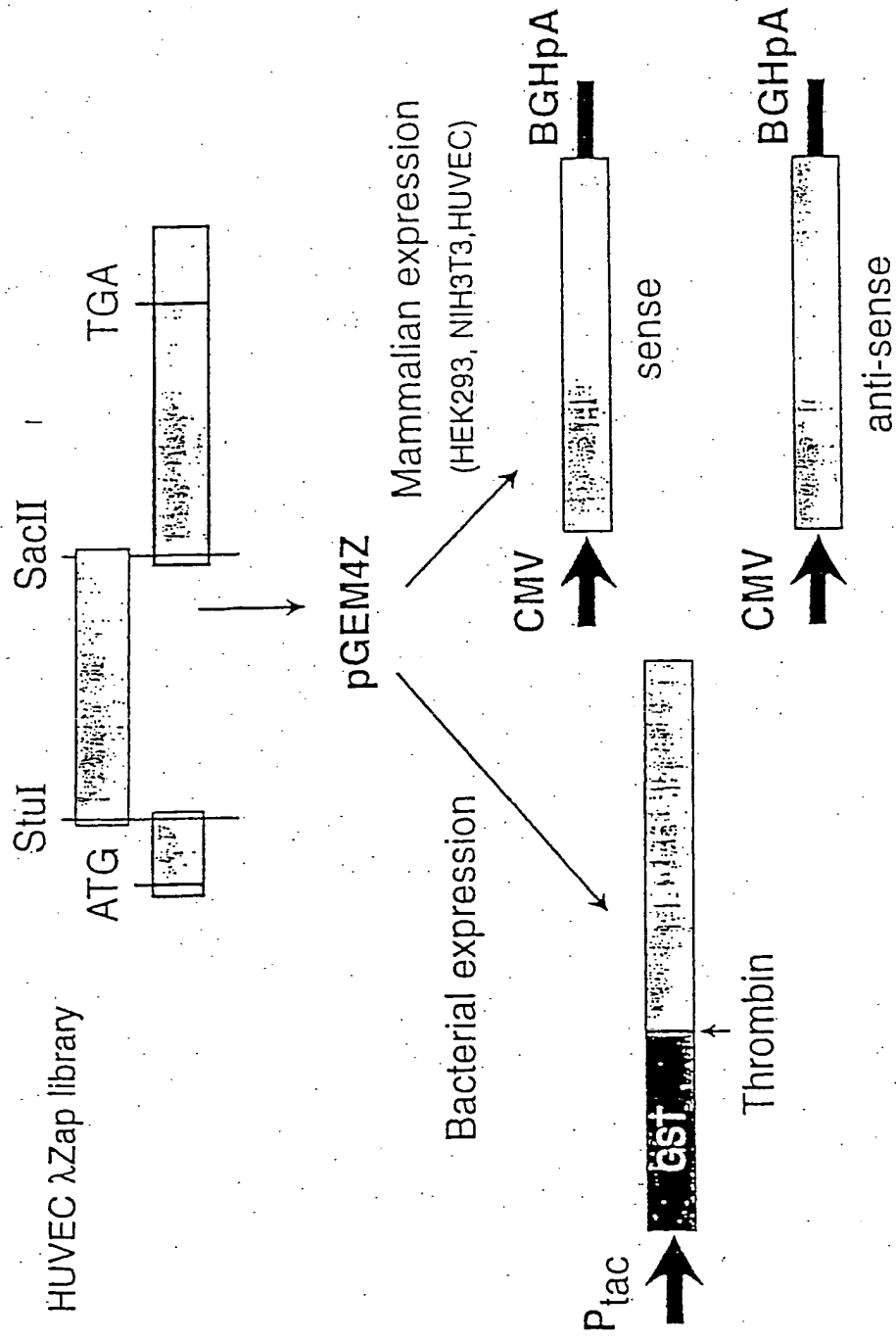


Figure 6

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1      M D P A G G P R G V L P R P C R V L V      19
1 gagcgcgggtcaggttATGGATCCAGCGGGCGGGCGGTGCTCCCGCGCCCTGCCGGTGGTG      75

20 L L N P R G G K A L Q L F R S H V Q P L L A E      44
76 CTGCTGAACCCGCGGGCAAGGCCCTTGCAGCTCTCCGGAGTCACGTGCAGCCCCCTTTGGCTGAG      150

45 A E I S F T L M L T E R R N H A R E L V R S E E L      69
151 GCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGGGAACCAAGCGGGGAGCTGGTGGGTCGGAGGAGCTG      225

70 G R W D A L V V M S G D G L M H E V V N G L M E R      94
226 GGCCGCTGGGACGCTCTGGTGGTCATGTCTGGAGACGGGCTGATGACGAGGTGGTGAACGGCTCATGGAGCGG      300

95 P D W E T A I Q K P L C S L P A G S G N A L A A S      119
301 CCTGACTGGGAGACCGCCATCCAGAAGCCCCCTGTGTAGCCTCCAGCAGGCTCTGGCAACGGCTGGCAGCTTCC      375

120 L N H Y A G Y E Q V T N E D L L T N C T L L L C R      144
376 TTGAACCATTAATGCTGGCTATGAGCAGGTACCAATGAAGACCTCCTGACCAACTGCACGCTATTGCTGTGCCCG      450

145 R L L S P M N L L S L H T A S G L R L F S V L S L      169
451 CGGCTGCTGTACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGGGCTGCCCTCTCTGTGCTCAGCCTG      525

170 A W G F I A D V D L E S E K Y R R L G E M R F T L      194
526 GCCTGGGGCTTCAATGCTGATGTGGACCTAGAGAGTGAGAAAGTATCGGCGTCTGGGGGAGATGCCGCTTCACTCTG      600

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Figure 7A-1

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195 G T F L R L A A L R T Y R G R L A Y L P V G R V G 219
601 GGCACCTTCCCTGCGTCTGGCAGCCTTGGCAGCCTTACCGGGCCGACTGGCTTACCTCCCTGTAGGAAGAGTGGGT 675

220 S K T P A S P V V V Q Q G P V D A H L V P L E E P 244
676 TCCAAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCCACTGGAGGAGCCA 750

245 V P S H W T V V P D E D F V L V L A L L H S H L G 269
751 GTGCCCCCTCACTGGACAGTGGTGCCCGACGAGGACTTGTGCTAGTCTCTGGCACTGCTGCACCTGCACCTGGGC 825

270 S E M F A A P M G R C A A G V M H L F Y V R A G V 294
826 AGTGAGATGTTGTGTGCACCCATGGCCCGCTGTGCAGCTGGCGTCATGCTGTCTTCTACGTGCGGGCGGGAGTG 900

295 S R A M L L R L F L A M E K G R H M E Y E C P Y L 319
901 TCTCGTGCCATGCTGCTGGCCCTCTTCCCTGGCCATGGAGAAGGCAGGCATATGGAGTATGAATGCCCCCTACTTG 975

320 V Y V P V V A F R L E P K D G K G M F A V D G E L 344
976 GTATATGTGCCCCGTGCTGCGCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTATGTTTGCAGTGGATGGGGAATTG 1050

345 M V S E A V Q G Q V H P N Y F W M V S G C V E P P 369
1051 ATGGTTAGCGAGGCCCGTGCAGGGCCAGGTGCACCCCAAACTACTTCTGGATGGTCAGCGGTTGCGTGAGCCCCCG 1125

370 P S W K P Q Q M P P P E E P L . 384
1126 CCCAGCTGGAAGCCCCCAGCAGATGCCACCGCCAGAAAGCCCTTatga 1173

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Figure 7A-2



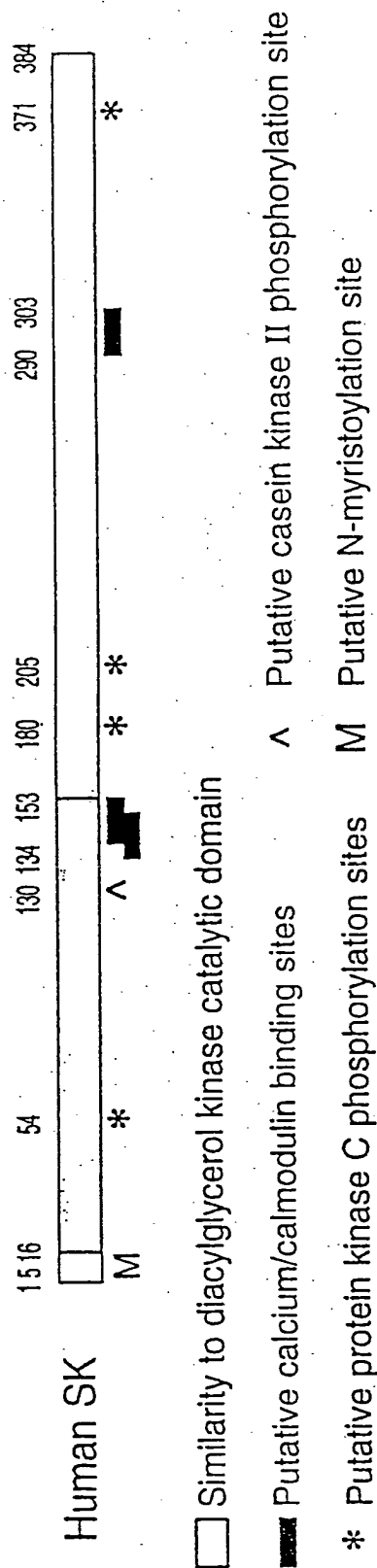
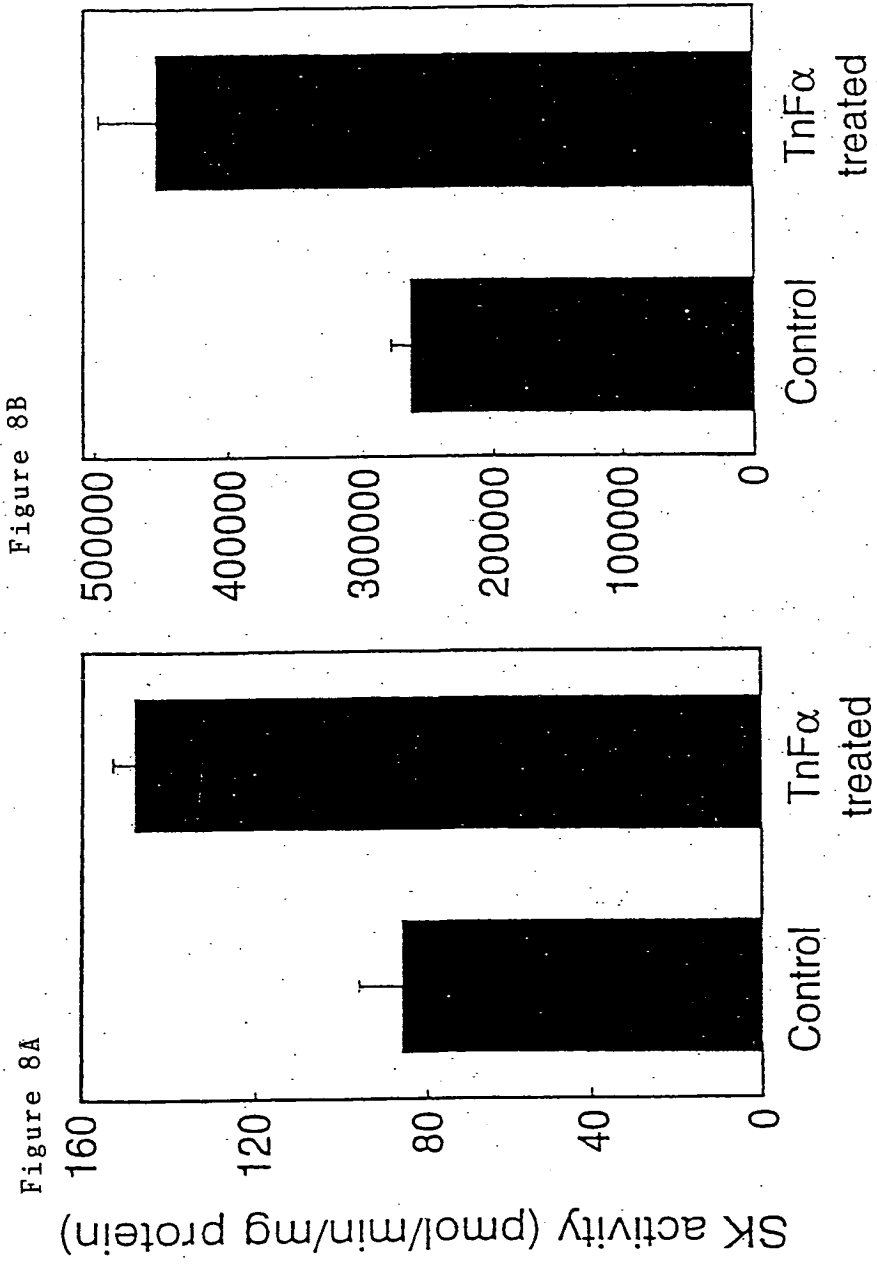


Figure 7B



hSK	1	.....MDPAGGPRGVLP	PCRVLV	LLNPR	<b>GGKGKALQL</b>	<b>FRSHVQPL</b>	<b>LAEA</b> EIS				
mSK1a	1	.....MEPECPRGLL	PCRVLV	LLNPQ	<b>GGKGKALQL</b>	<b>FQSRVQPF</b>	<b>LEEA</b> EIT				
mSK1b	1	MWCCVL	FVVECP	RGLL	PCRVLV	LLNPQ	<b>GGKGKALQL</b>	<b>FQSRVQPF</b>	<b>LEEA</b> EIT		
Yeast LCB4	206	NIS	SGTVEE	ILEKSY	ENSKR	NR	SILV	IINPH	<b>GGKGTA</b> KNL	<b>FLTKARPI</b>	<b>LVES</b> CGK
Yeast LCB5	252	DL...	VEEIL	KRSY	KNTR	RNKS	SIFV	IINPF	<b>GGKGKA</b> KKL	<b>EMTKAKPL</b>	<b>LASR</b> CS
S: pombe	90	....	FCEYLL	DVAY	KGIK	RSRR	FIV	FINPH	<b>GGKGKA</b> KKH	<b>WESEAE</b>	<b>PVFSSA</b> HSI
C. elegans	63	ENEQL	TSVIL	SRKPP	QEQCR	GNLL	VFINP	NSG	<b>TGKSLE</b>	<b>TANTVGPK</b>	<b>L</b> DKSLIR
Consensus		.....*	.....R	...*	*V	*NP	GGKGKA	..*	*F	*..*	P..*
hSK	112	<b>SGNALAA</b> S	LNHYA	GVEQ	VTNE	DL	TNCT	<b>LL</b> LCRR	...LL	<b>SPM</b> NLL	<b>SLHTAS</b> GLRL
mSK1a	111	<b>SGNALAA</b> S	VNHYA	GVEQ	VTNE	DL	LINCT	<b>LL</b> LCRR	...RL	<b>SPM</b> NLL	<b>SLHTAS</b> GLRL
mSK1b	118	<b>SGNALAA</b> S	VNHYA	GVEQ	VTNE	DL	LINCT	<b>LL</b> LCRR	...RL	<b>SPM</b> NLL	<b>SLHTAS</b> GLRL
Yeast LCB4	325	<b>SGNA</b> MSIS	.....	CHWT	NNPS	YAA	CLVKS	IE	TRID	<b>LMCCSQ</b>	<b>PSYMNE</b> WPR
Yeast LCB5	368	<b>SGNA</b> MSVS	.....	CHWT	NNPS	YST	CLIKS	IE	TRID	<b>LMCCSQ</b>	<b>PSYARE</b> HPK
S: pombe	203	<b>SGNA</b> AFSYN	.....	ATG	QLKP	ALTA	<b>LEILK</b>	GRPT	SFDL	<b>MTFEQ</b>	...KGKKA
C. elegans	184	<b>SGNGLLC</b> SV	..LSKY	GTKM	NEKSV	MERA	<b>LEIAT</b>	SPTA	KAES	VALY	<b>SVKTDNQ</b> .SY
Consensus		<b>SGNA</b> *..S	.....	.....	.....	.....	.....	.....	.....	.....	.....M

Figure 9A

hSK	211	.....AYLP.....	VGRVGSKTPASPVVVQQGPVD
mSK1a	210	.....AYLP.....	VGTVASKRPAST.LVQKGPVD
mSK1b	217	.....AYLP.....	VGTVASKRPAST.LVQKGPVD
Yeast LCB4	435	ENKDKNKGCLTFEP...NPSNSSPDLLSKNNINNSTKDE.....	
Yeast LCB5	478	EH...KNKGSLEFQHI TMNKDNEDCDNYNYENEYETENEDEDADDED SHLIS	
S. pombe	308	.....EKSKNLAPMSESSDSK.....	
C. elegans	284	.....TYRPPYKPKGFHPSSNVFSVYEKTTQQRIDDSKVKTNGSVSDSEETME	
Consensus		.....*	
hSK	282	AGVMHLFYV..RAGVSRAMLRLRLFLAMEKGRHMEYEC	PYL VYVPVVAFRLEPKDG
mSK1a	280	AGVMHLFYV..RAGVSR AALLRLFLAMQKGKHMELDC	PYL VHVVPVVAFRLEPRSQ
mSK1b	287	AGVMHLFYV..RAGVSR AALLRLFLAMQKGKHMELDC	PYL VHVVPVVAFRLEPRSQ
Yeast LCB4	532	DGTIDLVT DARIPVTR..MTPILLSLDKGS	..VLEPEVIH SKILAYKIIIPKVE
Yeast LCB5	586	DGTMDMVT DARTSLTR..MAPILLGLDKGS	..VLQPEVLH SKILAYKIIIPKLG
S. pombe	367	DGLIDVVI VYSKQFRKS..LLSMFTQLDNGGF..YYSKHLNYYKVRSFRFT	PVNT
C. elegans	388	DNRHLSYILWKDIGTRVNIAKYLLAIEHETELDL..PFVKHVEVSSMKLEVISE	
Consensus		G.*.....*.....*R.....*L**..G.H.....P.*.....*.....*.....P.*.....*	

Figure 9B

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FTLMLTERRNHARE.LVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAI.QKPLCSLPAG
FKLILTERKNHARE.LVCAEELGHWDALAVMSGDGLMHEVVNGLMERPDWETAI.QKPLCSLPGG
FKLILTERKNHARE.LVCAEELGHWDALAVMSGDGLMHEVVNGLMERPDWETAI.QKPLCSLPGG
IEIAYTKYARHAID.IAKDLDISKYDTIACASSGDGIPEYEVINGLYRRPDRVDAFNKLAVTQLPCG
IEVYTKYPGHAIE.IAREMDIDKYDTIACASSGDGIPEYEVINGLYRRPDRVDAFNKLAVTQLPCG
CEVLTTRRKDHAKS.IAKNLDVGSYDGILSVGGDGLFHEVINGLYRRPDRVDAFNKLAVTQLPCG
YEVVVTGPNHARNVMTKADLGKFNGLVILSGDGLVFEALNGILCREDAFRIFPTLPIGIVPSG
...T....HA.*.*.*.*D.*.*SGDG*.EV*NGL..R.D...A...*.*.*P.G

FVLSLAWGFIAVDVDLESEKYRR.LGEMRFTLGTFRLAALRTYRGRLL.....
YSVLSLSWGFVADVDLESEKYRR.LGEIRFTVGTFFRLASLRIYQGQL.....
YSVLSLSWGFVADVDLESEKYRR.LGEIRFTVGTFFRLASLRIYQGQL.....
LSFLSQTYGVIAESDINTE.FIRWMPVRFNLGVAFNIIQGGKYPCFVFKYAAKSKKELKVHFL
LSFLSQTYGLIAETDINTE.FIRWMPARFELGVAFNIIQGGKYPCFVFKYAAKSKNELKNHYL
YSFLTANYGIIADCDIGTE.NWRFMGENRAYLGFFLRLFOKPDWKCSIEMDVVSSDRTEIKHMY.
ASFLSIGWGLMADIDIDSEKWRKSLGHFRFTVMGFIRSCNLSRYKGRLL.....
.S.LS.**G.*A*.D***E.*R.*G..RF.*G.....*Y...*.....

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Figure 9C

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AHLVPLEEPVPSHW.....TVVPD.....EDFVLVLALLHSHLGSEMFAAPPMGRCA
THLVPLEEPVPSHW.....TVVPE.....QDFVLVLVLLHLLHSHLSSELFAPPMGRCE
THLVPLEEPVPSHW.....TVVPE.....QDFVLVLVLLHLLHSHLSSELFAPPMGRCE
.....LSPNFLNEDNFKLYPMTPEVPRDWKMDSELTDNLTIFYTGKMPYIAKDTKFFPAALPA
RDLADSSADQIKEEDFKIKYPLDEGIPSDWERLDPNISNNLGIFYTGKMPYVAAADTKFFPAALPS
.....TVSTSPESHLLTFEI.NDLSIFCAGLLPYIAPDAKMFPAASND
TKFQNWTLPDSDETLAVGSSDLEETVVIE.....DNFVNIYAVTLSHIAADGPPFAPSAKLE
.....**.....**.....*.....*.....*.....*.....*.....*.....P.....

KG..MFAVDGELMVSEAVQGQVHPNYFW.MVSGCVEPPSWKPQQMPPPEEPL identity 81%
RG..VFSVDGELMVCEAVQGQVHPNYLW.MVCGSRDAPSGRDSRRGPPPEEP. 80%
RG..VFSVDGELMVCEAVQGQVHPNYLW.MVCGSRDAPSGRDSRRGPPPEEP. 28%
SG..LFSVDGEEKFPLEPLQVEIMPMLCKTLLRNGRYIDTEFESM..... 30%
NG..LFSVDGEEKFPLEPLQVEIMPRLCKTLLRNGRYVDTDFDSM..... 30%
GKRHYFALDGESYPLEPFECRVAPPKLGTTLSPVAGFQLLDI..... 30%
GS..HVVLDGEVVDTKTIEVASTKNHIS.VFSSTA.....
*...F**DGE...E***...*P.....*.....*.....

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Figure 9D

Figure 10A

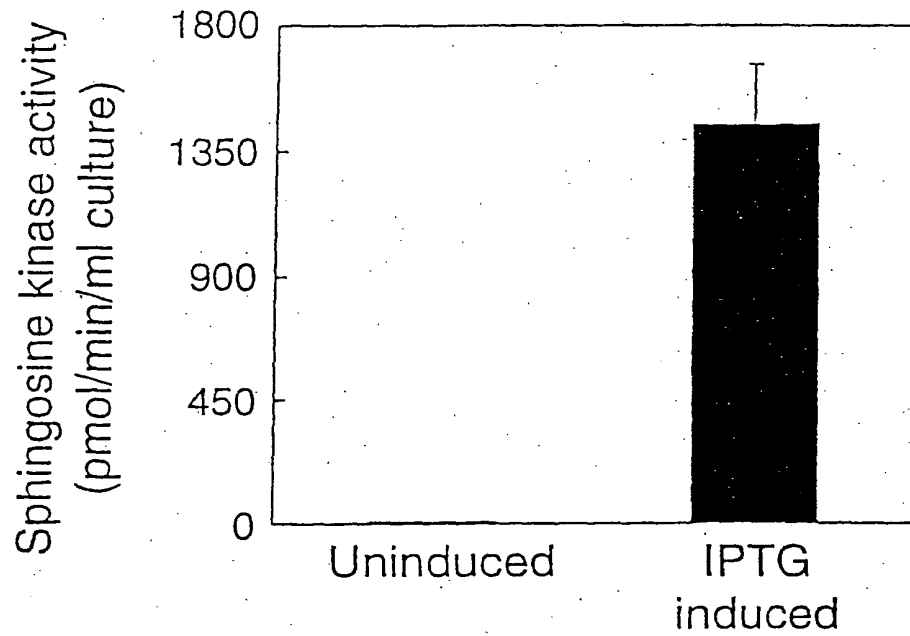


Figure 10B

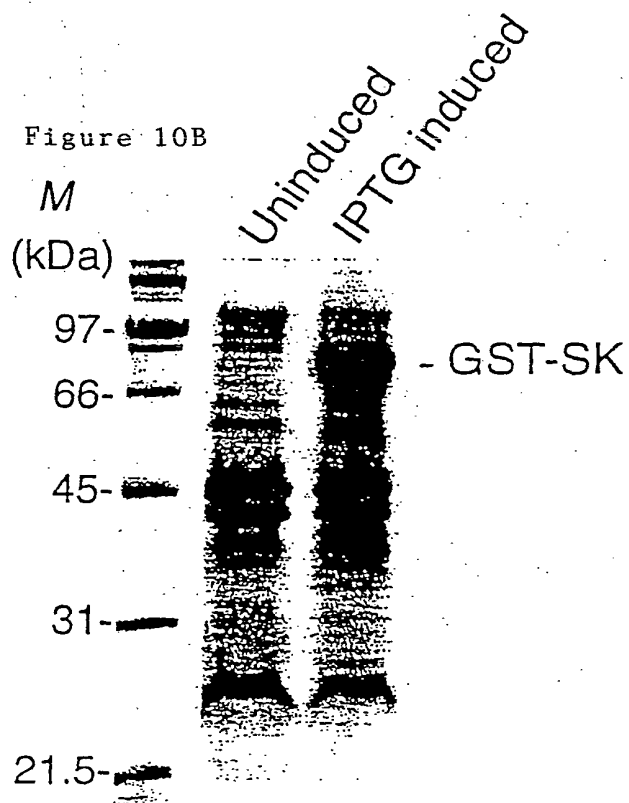
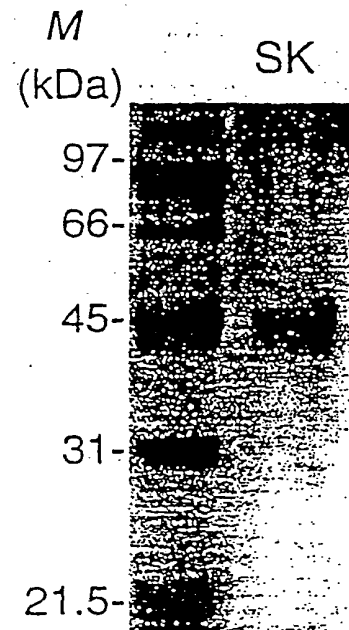


Figure 10C



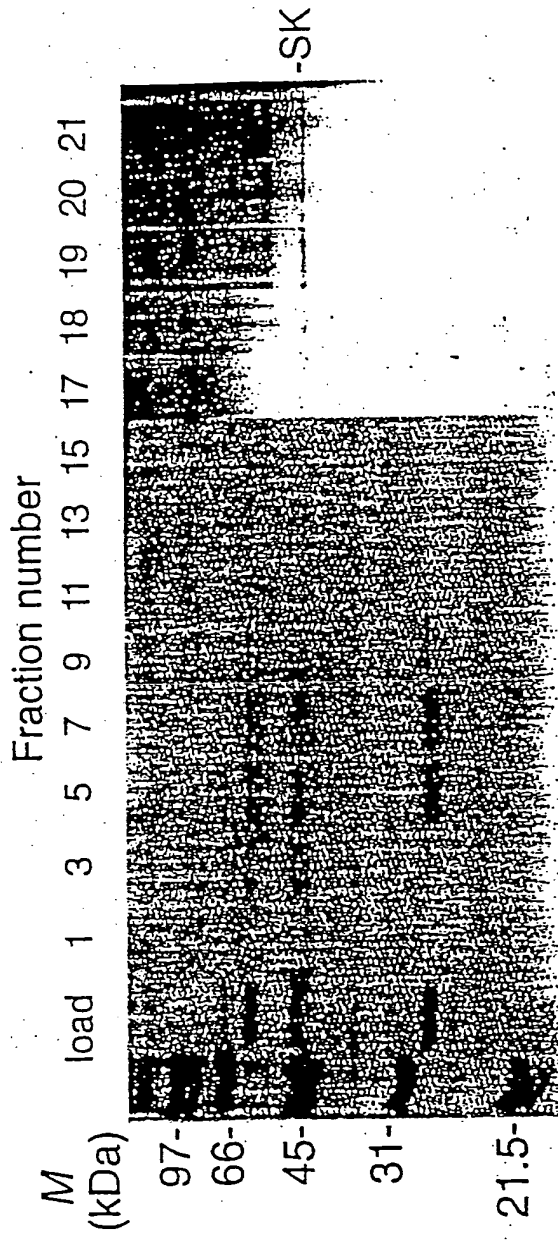


Figure 11A

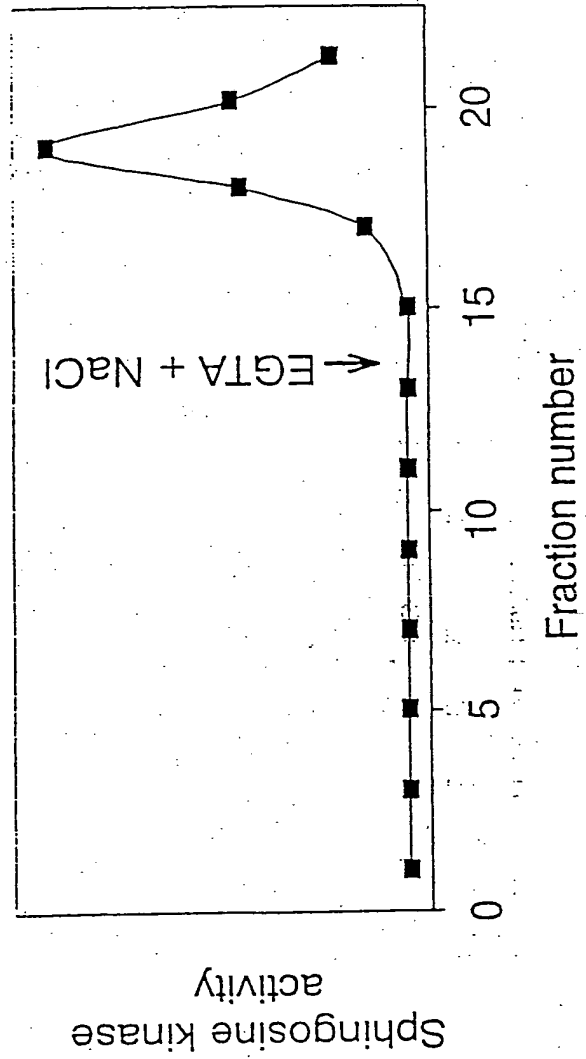


Figure 11B



Figure 12A

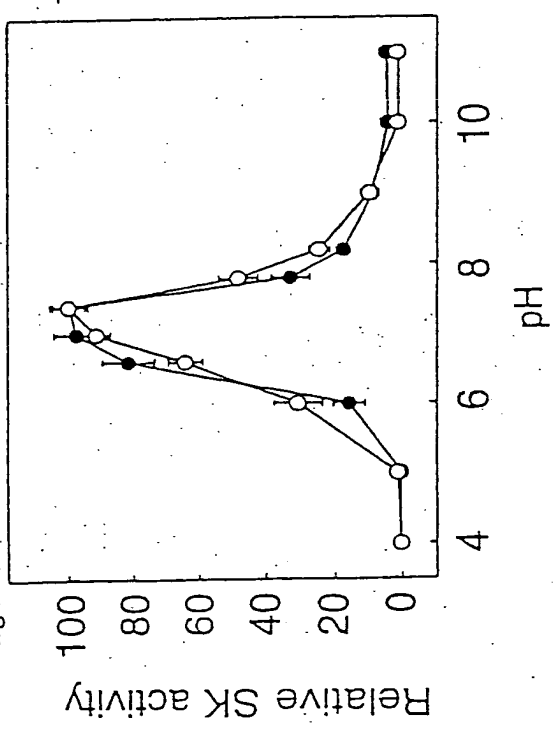


Figure 12B

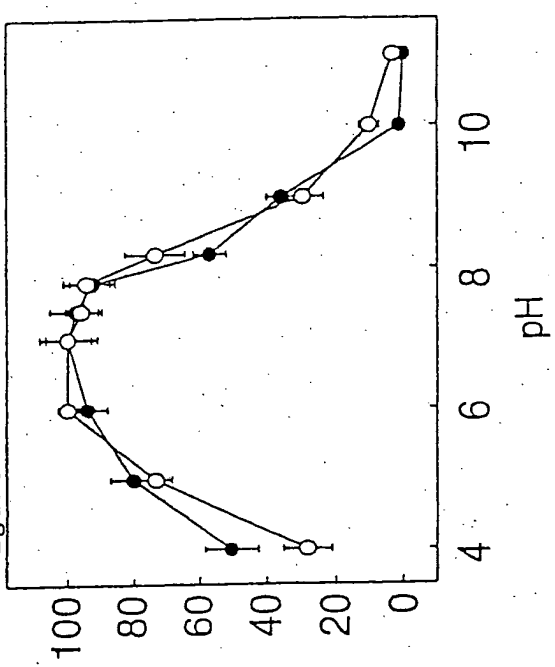


Figure 12C

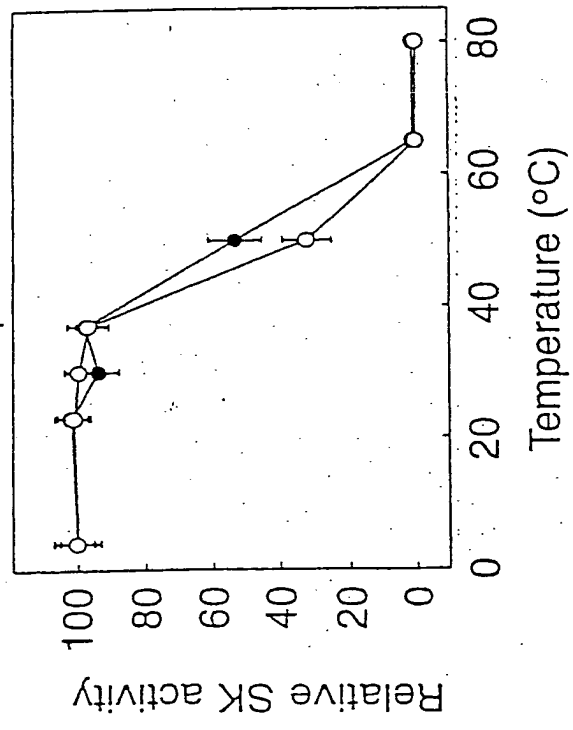
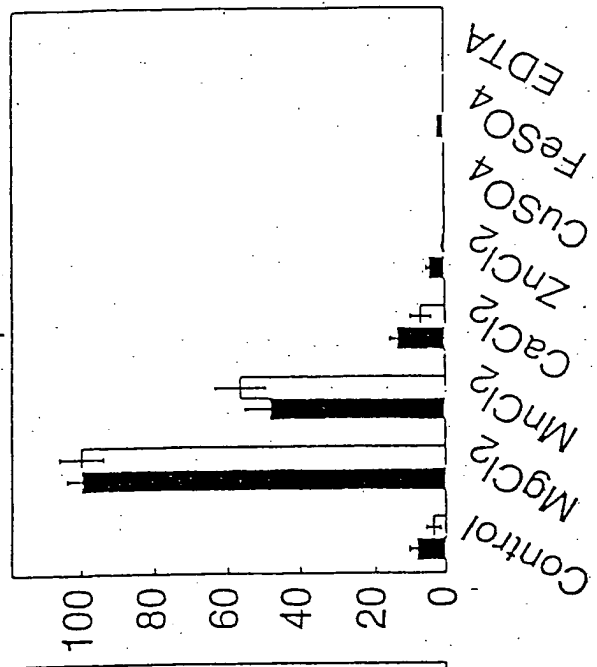
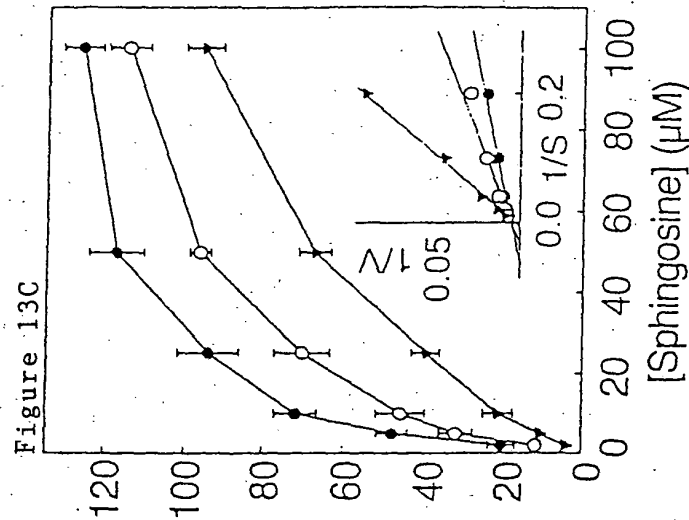
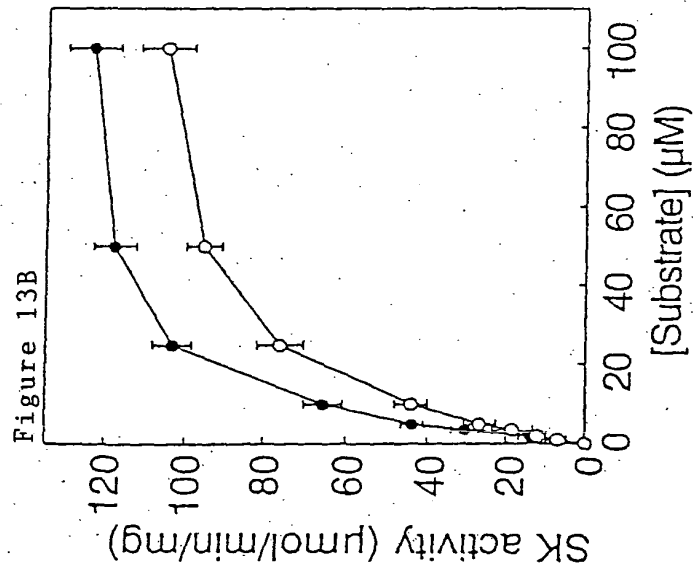
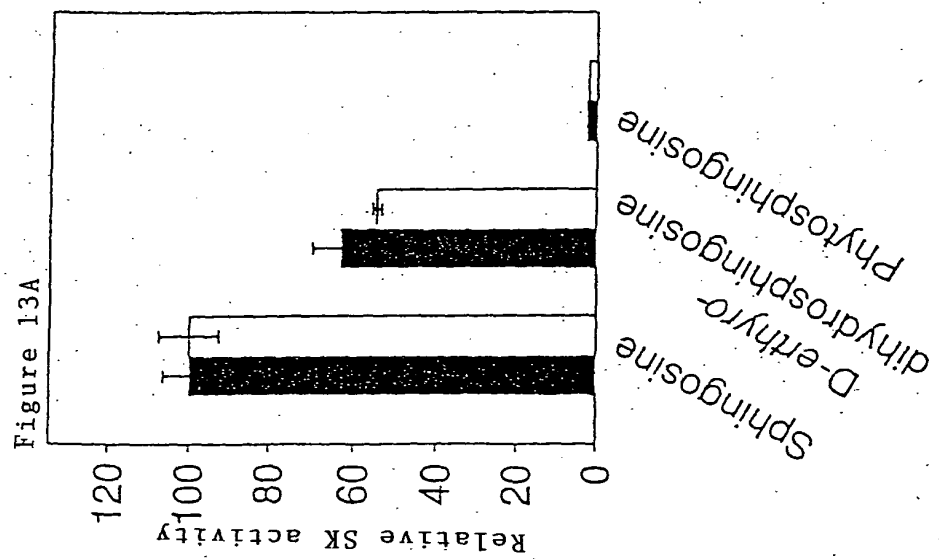


Figure 12D





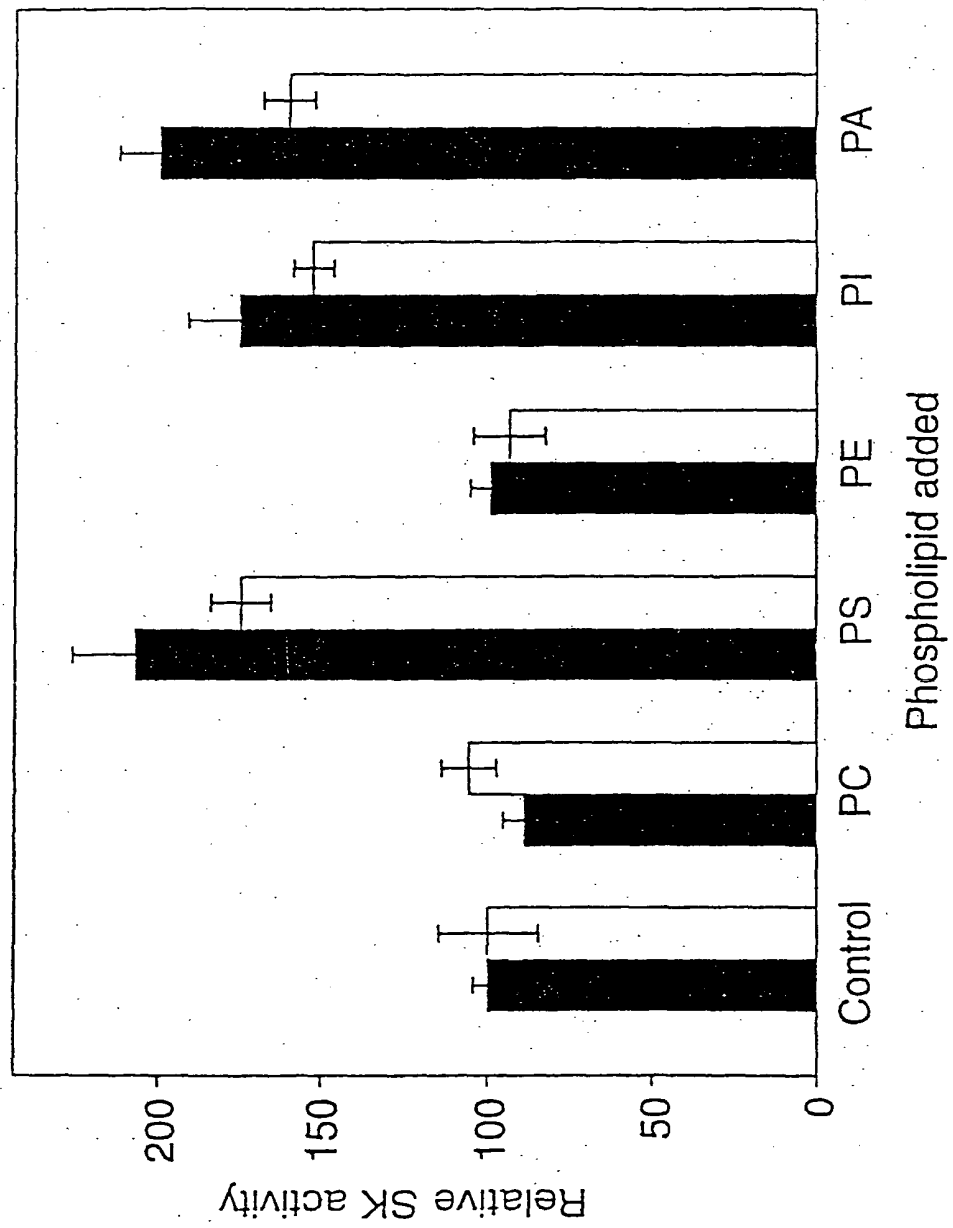


Figure 14